

0420

01-09-01

OIPF

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/729,264

DATE: 12/19/2000  
 TIME: 07:27:30

Input Set : A:\A-692.ST25.txt  
 Output Set: N:\CRF3\12192000\I729264.raw

#3/08  
 4/21/01  
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3 <110> APPLICANT: WELCHER, ANDREW  
 4 SARMIENTO, ULLA  
 5 SCHULTZ, HENRY  
 6 CHUTE, HILARY  
 8 <120> TITLE OF INVENTION: B7-LIKE MOLECULES AND USES THEREOF  
 10 <130> FILE REFERENCE: A-692  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/729,264  
 13 <141> CURRENT FILING DATE: 2000-11-28  
 15 <150> PRIOR APPLICATION NUMBER: US 60/214,512  
 16 <151> PRIOR FILING DATE: 2000-06-28  
 18 <160> NUMBER OF SEQ ID NOS: 15  
 20 <170> SOFTWARE: PatentIn version 3.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1175  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (27)..(1172)  
 31 <400> SEQUENCE: 1  
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 33 Met Gly Leu Val Ile Phe Leu His Gly  
 34 1 5  
 36 tct ggg tct ggt aat gaa gtc ata gaa ggc ccc cag aat gca aca gtc 101  
 37 Ser Gly Ser Gly Asn Glu Val Ile Glu Gly Pro Gln Asn Ala Thr Val  
 38 10 15 20 25  
 40 ctg aag ggc tcc cag gct cgc ttc aac tgc acc gtc tcc cag ggc tgg 149  
 41 Leu Lys Gly Ser Gln Ala Arg Phe Asn Cys Thr Val Ser Gln Gly Trp  
 42 30 35 40  
 44 aag ctc atc atg tgg gct ctc agt gac atg gtg gtg cta agc gtc agg 197  
 45 Lys Leu Ile Met Trp Ala Leu Ser Asp Met Val Val Leu Ser Val Arg  
 46 45 50 55  
 48 ccc atg gag ccc atc atc acc aat gac cgc ttc acc tct cag agg tac 245  
 49 Pro Met Glu Pro Ile Ile Thr Asn Asp Arg Phe Thr Ser Gln Arg Tyr  
 50 60 65 70  
 52 gac cag ggc ggg aac ttc acc tgc gag atg atc atc cac aat gtg gag 293  
 53 Asp Gln Gly Gly Asn Phe Thr Ser Glu Met Ile Ile His Asn Val Glu  
 54 75 80 85  
 56 ccc agt gat tgc ggg aac atc aga tgc agc ctc cag aac agt cgc ctg 341  
 57 Pro Ser Asp Ser Gly Asn Ile Arg Cys Ser Leu Gln Asn Ser Arg Leu  
 58 90 95 100 105  
 60 cat gga tct gct tac ctt acc gtc caa gtt atg gga gag ctg ttc att 389  
 61 His Gly Ser Ala Tyr Leu Thr Val Gln Val Met Gly Glu Leu Phe Ile  
 62 110 115 120  
 64 ccc agt gtt aat ctt gta gtc gct gag aat gaa cct tgt gaa gtt act 437  
 65 Pro Ser Val Asn Leu Val Val Ala Glu Asn Glu Pro Cys Glu Val Thr  
 66 125 130 135

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68 tgt cta ccc tca cac tgg acc cgg ctc ccg gat att tcc tgg gag ctc      485
69 Cys Leu Pro Ser His Trp Thr Arg Leu Pro Asp Ile Ser Trp Glu Leu
70          140          145          150
72 ggt ctc ctg gtc agc cat tca agc tat tat ttt gtt ccg gag ccc agc      533
73 Gly Leu Leu Val Ser His Ser Ser Tyr Tyr Phe Val Pro Glu Pro Ser
74          155          160          165
76 gac ctt caa agt gca tlg agc atc ctg gct ctg acc cca cag agc aat      581
77 Asp Leu Gln Ser Ala Val Ser Ile Leu Ala Leu Thr Pro Gln Ser Asn
78 170          175          180          185
80 ggg act ttg act tgc gtg gct acc tgg aag agc ctg aag gcc cgc aag      629
81 Gly Thr Leu Thr Cys Val Ala Thr Trp Lys Ser Leu Lys Ala Arg Lys
82          190          195          200
84 tct gca act gta aat ctc act gtg att ccg tgt ccc caa gac act gga      677
85 Ser Ala Thr Val Asn Leu Thr Val Ile Arg Cys Pro Gln Asp Thr Gly
86          205          210          215
88 qgt ggt att aat att cca ggt gta tta tca agt tta ccg agt tta ggt      725
89 Gly Gly Ile Asn Ile Pro Gly Val Leu Ser Ser Leu Pro Ser Leu Gly
90          220          225          230
92 ttt tca ttg cct act tgg ggc aaa gtt gga ctt gga cta gca ggc acc      773
93 Phe Ser Leu Pro Thr Trp Gly Lys Val Gly Leu Gly Leu Ala Gly Thr
94          235          240          245
96 atg ctt ctg acg ccg acg ggt act ctt aca ata cgc tgc tgc tgc tgc      821
97 Met Leu Leu Thr Pro Thr Cys Thr Leu Thr Ile Arg Cys Cys Cys Cys
98 250          255          260          265
100 cgc cgt cgt tgt tgt ggc tgc aac tgc tgc tgc cgt tgt tgc ttc tgc      869
101 Arg Arg Arg Cys Cys Gly Cys Asn Cys Cys Cys Arg Cys Cys Phe Cys
102          270          275          280
104 tgt aga aqa aaa aqa gga ttt cgt att caa ttt caa aag aaa tct gaa      917
105 Cys Arg Arg Lys Arg Gly Phe Arg Ile Gln Phe Gln Lys Lys Ser Glu
106          285          290          295
108 aaa gag aag aca aac aaa gaa act gag aca gaa agt gga aat gaa aac      965
109 Lys Glu Lys Thr Asn Lys Glu Thr Glu Thr Glu Ser Gly Asn Glu Asn
110          300          305          310
112 tcc ggc tac aat tca gat gaa caa aag acc aca gac acc gct tct ctc      1013
113 Ser Gly Tyr Asn Ser Asp Glu Gln Lys Thr Thr Asp Thr Ala Ser Leu
114          315          320          325
116 cct ccc aaa tcc tgt gaa tcc agt gat cct gaa caa aga aac agt agc      1061
117 Pro Pro Lys Ser Cys Glu Ser Ser Asp Pro Glu Gln Arg Asn Ser Ser
118 330          335          340          345
120 tgt ggc cct cct cac cag cgg gct gat caa cgt cca ccc agg cca gca      1109
121 Cys Gly Pro Pro His Gln Arg Ala Asp Gln Arg Pro Pro Arg Pro Ala
122          350          355          360
124 agt cat cca cag gct tct ttt aat ctg gcc agt cct gag aag gtc agt      1157
125 Ser His Pro Gln Ala Ser Phe Asn Leu Ala Ser Pro Glu Lys Val Ser
126          365          370          375
128 aat aca act gta gta tag      1175
129 Asn Thr Thr Val Val
130          380
133 <210> SEQ ID NO: 2

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134 &lt;211&gt; LENGTH: 382

135 &lt;212&gt; TYPE: PRT

136 &lt;213&gt; ORGANISM: Homo sapiens

138 &lt;400&gt; SEQUENCE: 2

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140 Met Gly Leu Val Ile Phe Leu His Gly Ser Gly Ser Gly Asn Glu Val
141 1 5 10 15
144 Ile Glu Gly Pro Gln Asn Ala Thr Val Leu Lys Gly Ser Gln Ala Arg
145 20 25 30
148 Phe Asn Cys Thr Val Ser Gln Gly Trp Lys Leu Ile Met Trp Ala Leu
149 35 40 45
152 Ser Asp Met Val Val Leu Ser Val Arg Pro Met Glu Pro Ile Ile Thr
153 50 55 60
156 Asn Asp Arg Phe Thr Ser Gln Arg Tyr Asp Gln Gly Gly Asn Phe Thr
157 65 70 75 80
160 Ser Glu Met Ile Ile His Asn Val Glu Pro Ser Asp Ser Gly Asn Ile
161 85 90 95
164 Arg Cys Ser Leu Gln Asn Ser Arg Leu His Gly Ser Ala Tyr Leu Thr
165 100 105 110
168 Val Gln Val Met Gly Glu Leu Phe Ile Pro Ser Val Asn Leu Val Val
169 115 120 125
172 Ala Glu Asn Glu Pro Cys Glu Val Thr Cys Leu Pro Ser His Trp Thr
173 130 135 140
176 Arg Leu Pro Asp Ile Ser Trp Glu Leu Gly Leu Leu Val Ser His Ser
177 145 150 155 160
180 Ser Tyr Tyr Phe Val Pro Glu Pro Ser Asp Leu Gln Ser Ala Val Ser
181 165 170 175
184 Ile Leu Ala Leu Thr Pro Gln Ser Asn Gly Thr Leu Thr Cys Val Ala
185 180 185 190
188 Thr Trp Lys Ser Leu Lys Ala Arg Lys Ser Ala Thr Val Asn Leu Thr
189 195 200 205
192 Val Ile Arg Cys Pro Gln Asp Thr Gly Gly Gly Ile Asn Ile Pro Gly
193 210 215 220
196 Val Leu Ser Ser Leu Pro Ser Leu Gly Phe Ser Leu Pro Thr Trp Gly
197 225 230 235 240
200 Lys Val Gly Leu Gly Leu Ala Gly Thr Met Leu Leu Thr Pro Thr Cys
201 245 250 255
204 Thr Leu Thr Ile Arg Cys Cys Cys Cys Arg Arg Arg Cys Cys Gly Cys
205 260 265 270
208 Asn Cys Cys Cys Arg Cys Cys Phe Cys Cys Arg Arg Lys Arg Gly Phe
209 275 280 285
212 Arg Ile Gln Phe Gln Lys Lys Ser Glu Lys Glu Lys Thr Asn Lys Glu
213 290 295 300
216 Thr Glu Thr Glu Ser Gly Asn Glu Asn Ser Gly Tyr Asn Ser Asp Glu
217 305 310 315 320
220 Gln Lys Thr Thr Asp Thr Ala Ser Leu Pro Pro Lys Ser Cys Glu Ser
221 325 330 335
224 Ser Asp Pro Glu Gln Arg Asn Ser Ser Cys Gly Pro Pro His Gln Arg
225 340 345 350
228 Ala Asp Gln Arg Pro Pro Arg Pro Ala Ser His Pro Gln Ala Ser Phe

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Input Set : A:\A-692.ST25.txt

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229          355          360          365
232 Asn Leu Ala Ser Pro Glu Lys Val Ser Asn Thr Thr Val Val
233          370          375          380
236 <210> SEQ ID NO: 3
237 <211> LENGTH: 1168
238 <212> TYPE: DNA
239 <213> ORGANISM: Homo sapiens
241 <220> FEATURE:
242 <221> NAME/KEY: CDS
243 <222> LOCATION: (8)..(1165)
245 <400> SEQUENCE: 3
246 agtgatc atg gtg gca gga gcc atg gaa aat aga gac cca ccc ggt tct      49
247          Met Val Ala Gly Ala Met Glu Asn Arg Asp Pro Pro Gly Ser
248          1          5          10
250 ggg tct ggt aat gaa gtc ata gaa ggc ccc caa aat gca aga gtc ctg      97
251 Gly Ser Gly Asn Glu Val Ile Glu Gly Pro Gln Asn Ala Arg Val Leu
252 15          20          25          30
254 aag ggc tcc cag gct cgc ttc aac tgc acc gtc tcc cag ggc tgg aag      145
255 Lys Gly Ser Gln Ala Arg Phe Asn Cys Thr Val Ser Gln Gly Trp Lys
256          35          40          45
258 ctc atc atg tgg gct ctc agt gac atg gtg gtg cta agc gtc agg ccc      193
259 Leu Ile Met Trp Ala Leu Ser Asp Met Val Val Leu Ser Val Arg Pro
260          50          55          60
262 atg gag ccc atc atc acc aat gac cgc ttc acc tct cag agg tac gac      241
263 Met Glu Pro Ile Ile Thr Asn Asp Arg Phe Thr Ser Gln Arg Tyr Asp
264          65          70          75
266 cag ggc ggg aac ttc acc tcg gag atg atc atc cac aat gtg gag ccc      289
267 Gln Gly Gly Asn Phe Thr Ser Glu Met Ile Ile His Asn Val Glu Pro
268          80          85          90
270 agt gat tcg ggg aac atc aga tgc agc ctc cag aac agt cgc ctg cat      337
271 Ser Asp Ser Gly Asn Ile Arg Cys Ser Leu Glu Asn Ser Arg Leu His
272 95          100          105          110
274 gga tct gct tac ctt acc gtc caa gtt atg gga gag ctg ttc att ccc      385
275 Gly Ser Ala Tyr Leu Thr Val Gln Val Met Gly Glu Leu Phe Ile Pro
276          115          120          125
278 agt gtt aat ctt gta gtc gct gag aat gaa cct tgt gaa gtt act tgt      433
279 Ser Val Asn Leu Val Val Ala Glu Asn Glu Pro Cys Glu Val Thr Cys
280          130          135          140
282 cta ccc tca cac tgg acc tgg ctc ccg gat att tcc tgg gag ctc ggt      481
283 Leu Pro Ser His Trp Thr Trp Leu Pro Asp Ile Ser Trp Glu Leu Gly
284          145          150          155
286 ctc ctg gtc agc cat tca agc tat tat ttt gtt ccg gag ccc agc gac      529
287 Leu Leu Val Ser His Ser Ser Tyr Tyr Phe Val Pro Glu Pro Ser Asp
288          160          165          170
290 ctt caa agt gca gtg agc atc ctg gct ctg acc cca cag agc aat ggg      577
291 Leu Gln Ser Ala Val Ser Ile Leu Ala Leu Thr Pro Gln Ser Asn Gly
292 175          180          185          190
294 act ttg act tgc gtg gct acc tgg aag agc ctg aag gcc cgc aag tct      625
295 Thr Leu Thr Cys Val Ala Thr Trp Lys Ser Leu Lys Ala Arg Lys Ser

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296          195          200          205
298 gca act gta aat ctc act gtg att cgg tgt ccc caa gac act gga ggt      673
299 Ala Thr Val Asn Leu Thr Val Ile Arg Cys Pro Gln Asp Thr Gly Gly
300          210          215          220
302 ggt att aat att cca ggt gta tta tca agt tta ccg agt tta ggt ttt      721
303 Gly Ile Asn Ile Pro Gly Val Leu Ser Ser Leu Pro Ser Leu Gly Phe
304          225          230          235
306 tca ttg cct act tgg ggc aaa gtt gga cta gca ggc acc atg      769
307 Ser Leu Pro Thr Trp Gly Lys Val Gly Leu Gly Leu Ala Gly Thr Met
308          240          245          250
310 ctt ctg acg ccg acg tgt act ctt aca ata cgc tgc tgc tgc tgc cgc      817
311 Leu Leu Thr Pro Thr Cys Thr Ile Arg Cys Cys Cys Cys Arg
312 255          260          265          270
314 cgt cgt tgt tgt ggc tgc aac tgc tgc tgc cgt tgt tgt ttc tgc tgt      865
315 Arg Arg Cys Cys Gly Cys Asn Cys Cys Arg Cys Cys Phe Cys Cys
316          275          280          285
318 aga aqa aaa aga gga ttt cgt att caa ttt caa aag aaa tct gaa aaa      913
319 Arg Arg Lys Arg Gly Phe Arg Ile Gln Phe Gln Lys Lys Ser Glu Lys
320          290          295          300
322 gag aag aca aac aaa gaa act gag aca gaa agt gga aat gaa aac tcc      961
323 Glu Lys Thr Asn Lys Glu Thr Glu Thr Glu Ser Gly Asn Glu Asn Ser
324          305          310          315
326 ggc tac aat tca gat gaa caa aag acc aca gac acc gct tct ctc cct      1009
327 Gly Tyr Asn Ser Asp Glu Gln Lys Thr Thr Asp Thr Ala Ser Leu Pro
328          320          325          330
330 ccc aaa tcc tgt gaa tcc agt gat cct gaa caa aga aac agt agr tgt      1057
331 Pro Lys Ser Cys Glu Ser Ser Asp Pro Glu Gln Arg Asn Ser Ser Cys
332 335          340          345          350
334 ggc cct cct cac cag cgg gct gat caa cgt cca ccc agg cca gca agt      1105
335 Gly Pro Pro His Gln Arg Ala Asp Gln Arg Pro Pro Arg Pro Ala Ser
336          355          360          365
338 cat cca caq gct tct ttt aat ctg gcc agt cct gag aag gtc agt aat      1153
339 His Pro Gln Ala Ser Phe Asn Leu Ala Ser Pro Glu Lys Val Ser Asn
340          370          375          380
342 aca act gta gta tag      1168
343 Thr Thr Val Val
344          385
347 <210> SEQ ID NO: 4
348 <211> LENGTH: 386
349 <212> TYPE: PRT
350 <213> ORGANISM: Homo sapiens
352 <400> SEQUENCE: 4
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355 1          5          10          15
358 Gly Asn Glu Val Ile Glu Gly Pro Gln Asn Ala Arg Val Leu Lys Gly
359          20          25          30
362 Ser Gln Ala Arg Phe Asn Cys Thr Val Ser Gln Gly Trp Lys Leu Ile
363          35          40          45
366 Met Trp Ala Leu Ser Asp Met Val Val Leu Ser Val Arg Pro Met Glu

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/729,264

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Input Set : A:\A-692.ST25.txt

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